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RAW SEQUENCE LISTING   DATE: 12/10/2002
PATENT APPLICATION: US/09/835,297A   TIME: 13:34:09

Input Set : A:\Seqlistcorrected.txt
Output Set: N:\CRF4\12102002\I835297A.raw

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 3 <110> APPLICANT: Bluestone, Jeffrey
 4        Collins, Mary
 5        Whitters, Matthew J.
 6        Kranz, David
 7        Griffin, Matthew D.
 9 <120> TITLE OF INVENTION: SURFACE-BOUND ANTIGEN BINDING PORTIONS OF ANTIBODIES
10        THAT BIND TO CTLA4 AND CD28 AND USES THEREFOR
12 <130> FILE REFERENCE: GNN-014CP
14 <140> CURRENT APPLICATION NUMBER: US 09/835297A
15 <141> CURRENT FILING DATE: 2001-04-12
17 <150> PRIOR APPLICATION NUMBER: US 60/196851
18 <151> PRIOR FILING DATE: 2000-04-12
20 <160> NUMBER OF SEQ ID NOS: 17
22 <170> SOFTWARE: PatentIn Ver. 2.0
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25 <211> LENGTH: 672
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
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32 gcccagcctg ctgtggtact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180
33 gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag 240
34 gtgactgaag tctgtgcggc aacctacatg acggggaatg agttgacctt cctagatgat 300
35 tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg 360
36 gccatggaca cgggactcta catctgcaag gtggagctca tgtacccacc gccatactac 420
37 ctgggcatag caacggaac ccagatttat gtaattgatc cagaaccgtg cccagattct 480
38 gacttcctcc tctggatcct tgcagcagtt agttcggggt tgttttttta tagctttctc 540
39 ctcacagctg tttctttgag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600
40 tatgtgaaaa tgcccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660
41 cccatcaatt ga                                                   672
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44 <211> LENGTH: 223
45 <212> TYPE: PRT
46 <213> ORGANISM: Homo sapiens
48 <400> SEQUENCE: 2
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52 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
53               20                  25                  30
55 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
56          35                  40                  45
58 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
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59        50                    55                    60
61 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
62   65                    70                    75                    80
64 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
65                    85                    90                    95
67 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
68              100                   105                   110
70 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
71          115                   120                   125
73 Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
74    .130                   135                   140
76 Asn Gly Ala Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
77 145                   150                   155                   160
79 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
80                   165                   170                   175
82 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
83              180                   185                   190
85 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
86          195                   200                   205
88 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
89    210                   215                   220
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92 <211> LENGTH: 3806
93 <212> TYPE: DNA
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 3
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98 tttgagtgcc ttgatcatgt gccctaaggg gatggtggcg gtggtggtgg ccgtggatga 120
99 cggagactct caggccttgg caggtgcgtc tttcagttcc cctcacactt cgggttcctc 180
100 ggggaggagg ggctggaacc ctagcccatc gtcaggacaa agatgctcag gctgctcttg 240
101 gctctcaact tattcccttc aattcaagta acaggaaaca agattttggt gaagcagtcg 300
102 cccatgcttg tagcgtacga caatgcggtc aaccttagct gcaagtattc ctacaatctc 360
103 ttctcaaggg agttccgggc atcccttcac aaaggactgg atagtgctgt ggaagtctgt 420
104 gttgtatatg ggaattactc ccagcagctt caggtttact caaaaacggg gttcaactgt 480
105 gatgggaaat tgggcaatga atcagtgaca ttctacctcc agaatttgta tgttaaccaa 540
106 acagatattt acttctgcaa aattgaagtt atgtatcctc ctccttacct agacaatgag 600
107 aagagcaatg gaaccattat ccatgtgaaa gggaaacacc tttgtccaag tcccctattt 660
108 cccggacctt ctaagccctt ttgggtgctg gtggtggttg gtggagtcct ggcttgctat 720
109 agcttgctag taacagtggc ctttattatt ttctgggtga ggagtaagag gagcaggctc 780
110 ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 840
111 cagccctatg ccccaccacg cgacttcgca gcctatcgct cctgacacgg acgcctatcc 900
112 agaagccagc cggctggcag cccccatctg ctcaatatca ctgctctgga taggaaatga 960
113 ccgccatctc cagccggcca cctcaggccc ctgttgggcc accaatgcca atttttctcg 1020
114 agtgactaga ccaaatatca agatcatttt gagactctga aatgaagtaa aagagatttc 1080
115 ctgtgacagg ccaagtctta cagtgccatg gcccacattc caacttacca tgtacttagt 1140
116 gacttgactg agaagttagg gtagaaaaca aaaagggagt ggattctggg agcctcttcc 1200
117 ctttctcact cacctgcaca tctcagtcaa gcaaagtgtg gtatccacag acattttagt 1260
118 tgcagaagaa aggctaggaa atcattcctt ttggttaaat gggtgtttaa tcttttggtt 1320
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120 attaaaacac tgtctcccac tcatgaaatg agccacgtag ttcctattta atgctgtttt 1440
121 cctttagttt agaaatacat agacattgtc ttttatgaat tctgatcata tttagtcatt 1500
122 ttgaccaaat gagggatttg gtcaaatgag ggattccctc aaagcaatat caggtaaacc 1560
123 aagttgcttt cctcactccc tgtcatgaga cttcagtgtt aatgttcaca atatactttc 1620
124 gaaagaataa aatagttctc ctacatgaag aaagaatatg tcaggaaata aggtcacttt 1680
125 atgtcaaaat tatttgagta ctatgggacc tggcgcagtg gctcatgctt gtaatcccag 1740
126 cactttggga ggccgaggtg ggcagatcac ttgagatcag gaccagcctg gtcaagatgg 1800
127 tgaaactccg tctgtactaa aaatacaaaa tttagcttgg cctggtggca ggcacctgta 1860
128 atcccagctg cccaggaggc tgaggcatga gaatcgcttg aacctggcag gcggaggttg 1920
129 cagtgagccg agatagtgcc acagctctcc agcctgggcg acagagtgag actccatctc 1980
130 aaacaacaac aacaacaaca acaacaacaa caaaccacaa aattatttga gtactgtgaa 2040
131 ggattatttg tctaacagtt cattccaatc agaccaggta ggagctttcc tgtttcatat 2100
132 gtttcagggt tgcacagttg gtctctttaa tgtcggtgtg gagatccaaa gtgggttgtg 2160
133 gaaagagcgt ccataggaga agtgagaata ctgtgaaaaa gggatgttag cattcattag 2220
134 agtatgagga tgagtcccaa gaaggttctt tggaaggagg acgaatagaa tggagtaatg 2280
135 aaattcttgc catgtgctga ggagatagcc agcattaggt gacaatcttc cagaagtggt 2340
136 caggcagaag gtgccctggt gagagctcct ttacagggac tttatgtggt ttagggctca 2400
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138 gtattttgga atgtgtcttt tgaagagagc atcagagttc ttaagggact gggtaaggcc 2520
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142 agttgaatag cctcaggcaa gtcactgccc acctaagatg atggttcttc aactataaaa 2760
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145 gctattggta ttattgccat atagataaat tatgtataaa aattaaactg ggcaatagcc 2940
146 taagaagggg ggaatattgt aacacaaatt taaacccact acgcagggat gaggtgctat 3000
147 aatatgagga ccttttaact tccatcattt tcctgtttct tgaaatagtt tatcttgtaa 3060
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149 tgtgagaagg aagggaggag taggaatctt gagattccag atcgaaaata ctgtactttg 3180
150 gttgattttt aagtgggctt ccattccatg gatttaatca gtcccaagaa gatcaaactc 3240
151 agcagtactt gggtgctgaa gaactgttgg atttaccctg gcacgtgtgc cacttgccag 3300
152 cttcttgggc acacagagtt cttcaatcca agttatcaga ttgtatttga aaatgacaga 3360
153 gctggagagt tttttgaaat ggcagtggca aataaataaa tacttttttt taaatggaaa 3420
154 gacttgatct atggtaataa atgattttgt tttctgactg gaaaaatagg cctactaaag 3480
155 atgaatcaca cttgagatgt ttcttactca ctctgcacag aaacaaagaa gaaatgttat 3540
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157 gagcaatgct ttcatagttt cagatatggt agttatgaag aaaacaatgt catttgctgc 3660
158 tattattgta agagtcttat aattaatggt actcctataa tttttgattg tgagctcacc 3720
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160 ttcagtgata aaattactaa actact                                      3806
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 220
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 4
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169   1               5                   10                  15
171 Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
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Input Set : **A:\Seqlistcorrected.txt**
Output Set: **N:\CRF4\12102002\I835297A.raw**

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172              20              25              30
174 Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
175         35              40              45
177 Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
178      50              55              60
180 Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
181 65              70              75              80
183 Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
184             85              90              95
186 Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
187         100             105             110
189 Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
190         115             120             125
192 Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
193      130             135             140
195 Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
196 145             150             155             160
198 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
199             165             170             175
201 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
202         180             185             190
204 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
205         195             200             205
207 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
208      210             215             220
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210 <210> SEQ ID NO: 5
211 <211> LENGTH: 16
212 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Linker region of fusion protein
218 <400> SEQUENCE: 5
219 Glu Ser Gly Ser Val Ser Ser Glu Glu Leu Ala Phe Arg Ser Leu Asp
220 1   5   10   15
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 34
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Primer for polymerase chain reaction
230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (15)
233 <223> OTHER INFORMATION: n = c or g
235 <220> FEATURE:
236 <221> NAME/KEY: misc_feature
237 <222> LOCATION: (21)
238 <223> OTHER INFORMATION: n = c or a
240 <220> FEATURE:

Input Set : A:\Seqlistcorrected.txt
Output Set: N:\CRF4\12102002\I835297A.raw

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       241 <221> NAME/KEY: misc_feature
       242 <222> LOCATION: (27)
       243 <223> OTHER INFORMATION: n = c or g or a
       245 <220> FEATURE:
       246 <221> NAME/KEY: misc_feature
       247 <222> LOCATION: (28)
       248 <223> OTHER INFORMATION: n = a or t
       250 <220> FEATURE:
       251 <221> NAME/KEY: misc_feature
       252 <222> LOCATION: (30)
       253 <223> OTHER INFORMATION: n = g or c
       255 <400> SEQUENCE: 6
W--> 256 cgaatgatgc atccnaggtg nagctgnngn agtc                    34
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       259 <211> LENGTH: 36
       260 <212> TYPE: DNA
       261 <213> ORGANISM: Artificial Sequence
       263 <220> FEATURE:
       264 <223> OTHER INFORMATION: primer for polymerase chain reaction
       266 <220> FEATURE:
       267 <221> NAME/KEY: misc_feature
       268 <222> LOCATION: (34)
       269 <223> OTHER INFORMATION: n = g or a
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       274 <210> SEQ ID NO: 8
       275 <211> LENGTH: 29
       276 <212> TYPE: DNA
       277 <213> ORGANISM: Artificial Sequence
       279 <220> FEATURE:
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       282 <400> SEQUENCE: 8
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       286 <211> LENGTH: 40
       287 <212> TYPE: DNA
       288 <213> ORGANISM: Artificial Sequence
       290 <220> FEATURE:
       291 <223> OTHER INFORMATION: primer for polymerase chain reaction
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       294 <221> NAME/KEY: misc_feature
       295 <222> LOCATION: (23)
       296 <223> OTHER INFORMATION: n = t or g
       298 <400> SEQUENCE: 9
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       301 <210> SEQ ID NO: 10
       302 <211> LENGTH: 93
       303 <212> TYPE: DNA
       304 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/10/2002
PATENT APPLICATION: **US/09/835,297A**   TIME: 13:34:10

Input Set : **A:\Seqlistcorrected.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 15,21,27,28,30
Seq#:7; N Pos. 34
Seq#:9; N Pos. 23

VERIFICATION SUMMARY   DATE: 12/10/2002
PATENT APPLICATION: **US/09/835,297A**   TIME: 13:34:10

Input Set : **A:\Seqlistcorrected.txt**
Output Set: **N:\CRF4\12102002\I835297A.raw**

L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0